

SEQUENCE LISTING

<110> DeVico et al, Anthony

<120> VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE

<130> 4115-144 CIP

<160> 33

<170> PatentIn version 3.1

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<211> 2159

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

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Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
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245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
325 330 335

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340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
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370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
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Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
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Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
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Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
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Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
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Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
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Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
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Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
 595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
 610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
 625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
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Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
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<213> Artificial Sequence

<220>
<223> Synthesized construct

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<210> 4
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 <222> (716)..(720)
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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys

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Glu	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala
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Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Ala	Met	Tyr	Ala	Pro
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Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
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Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys
515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
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Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
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Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
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Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
690 695 700

Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
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<211> 1668
<212> DNA
<213> Artificial Sequence

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gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg 240
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cccgccgggt tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc 720
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<211> 556
<212> PRT
<213> Artificial Sequence

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<221> MISC_FEATURE
<222> (1)..(556)
<223> X can be any amino acid

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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Cys
515 520 525

Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu Gly
530 535 540

Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro Xaa

Protein = 0947660

545

550

555

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 <211> 39
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 <221> primer
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 gcgctt 66

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 <222> (1)..(69)
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 aaaggggat 69

<210> 10
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<212>   DNA
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<220>
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195

200

205

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210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg
225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly
245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe
260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu
275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg
290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr
305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly
325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val
340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile Gly Ser Ser Gly Gly Gly Gly Ser
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys Lys Val
385 390 395 400

Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser
405 410 415

Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys
420 425 430

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 <212> DNA
 <213> Artificial Sequence

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<210> 20
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>
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 Gly Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro
 20 25

<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
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 aagtgcgccg gcagcttctg cgctgcggc ccctaagaat tc 102

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 <212> DNA
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<400> 22

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gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440
tacaaggtgg tgaagatcga gcccctgggc gtggcccca ccaaggcca gcgccgcgtg 1500
gtgcagcgcg agaagcgt 1518

<210> 24
<211> 506
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthesized construct
<400> 24

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn

00024050-03042600

160

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Arg
500 505

<210> 25
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 25
aagaaagtgg tgctgggcaa aaaaggggat acagtggaac tgacctgtac agcttcccag 60
aagaagagca tacaattcca ctggaaaaac tccaaccaga taaagattct gggaaatcag 120
ggctccttct taactaaagg tccatccaag ctgaatgac gcgctgactc aagaagaagc 180
ctttgggacc aaggaaactt cccctgatc atcaagaatc ttaagataga agactcagat 240
acttacatct gtgaagtgga ggaccagaag gaggaggtgc aattgctagt gttcggattg 300
actgccaact ctgacacca cctgcttcag gggcagagcc tgaccctgac cttggagagc 360
ccccctggta gtagccctc agtgcaatgt aggagtccaa ggggtaaaaa catacagggg 420

Leu Ala

<210> 27
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 27
atgcccatgg ggtctctgca accgctggcc accttgtacc tgctggggat gctgggtcgct 60
tcttgccctg gaaagaacgt gaccgagaac ttcaacatgt ggaagaacaa catgggtggag 120
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240
gcggggccgcc tgatcagctg caacaccagc gtgatcacc aggctgccc caaggtgagc 300
ttcgagccca tccccatcca ctactgcgc cccgcccggc tcgccatcct gaagtgaag 360
gacaagaagt tcaacggcaa gggcccctgc accaacgtga gcaccgtgca gtgcacccac 420
ggcatccgcc ccgtggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480
gtggtgatcc gcagcgccaa cttcgccgac aacgccaaagg tgatcatcgt gcagctgaac 540
gagagcgtgg agatcaactg caccgcgcc aacaacaaca cccgcaagtc catccacatc 600
ggccccggcc gcgccttcta caccaccggc gagatcatcg gcgacatccg ccaggcccac 660
tgcaacctga gccgcgccaa gtggaacgac accctgaaca agatcgtgat caagctgcgc 720
gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcggcga ccccgagatc 780
gtgaccacac gcttcaattg cggcggcgag ttcttctact gcaacagcac ccagctgttc 840
aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaacaa caccatcacc 900
ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtgggccc cgccatgtac 960
gcccccccca tccgcggcca gatccgctgc agttchaaca tcaccggcct gctgctgacc 1020
cgcgacggcg gccccgagga caacaagacc gaggtgttcc gccccggcgg cggcgacatg 1080
cgcgacaact ggcgcagcga gctgtacaag tacaaggtgg tgaagatc 1128

<210> 28
<211> 376
<212> PRT

[illegible]

<223> Synthesized construct

<400> 28

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Lys Asn Val Thr Glu Asn Phe Asn
20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser
35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
130 135 140

Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu
145					150					155					160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr
195 200 205

<223> Synthesized construct

<400> 30

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe

U944660 = 034301

220

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
435 440 445

SECRET

ALL INFORMATION CONTAINED
HEREIN IS UNCLASSIFIED
DATE 08-16-97 BY 6032 JRS/KJS

SECRET

<213> Artificial Sequence

<220>

<220>

<222> (1) . . (259)

<400> 32

Met Leu Val Ala Ser Val Leu Ala Asp Pro Glu Glu Pro Lys Ser Cys
20 25 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
35 40 45

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
50 55 60

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
65 70 75 80

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
85 90 95

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
100 105 110

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
115 120 125

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
130 135 140

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
145 150 155 160

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
165 170 175

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 180 185 190

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 195 200 205

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 210 215 220

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 225 230 235 240

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 245 250 255

Pro Gly Xaa

<210> 33
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<400> 33
 ggatcctctg gtggcggtgg ctctgggctcc ggaggaggtg ggtcgggtgg cggcgcggcc 60
 gct 63

TOE230-0304E060